ABSTRACT OF THE DESCRIPTION

Disclosed is a method of identifying genes that are over-expressed in adipose tissue as compared to pre-adipocyte tissue or other tissues comprising performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) from any two different mice selected from the group consisting of wild-type, HMGI-C -/-, ob/ob, and HMGI-C -/- ob/ob genotype mice. Based on this method a number of nucleotide sequences are identified whose expression is adipocyte specific. The identified nucleotide sequences and their corresponding polypeptides are then used to prevent adipogenesis, to treat diabetes, and to screen for small-molecules that can modulate or prevent adipogenesis and to treat diabetes.